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Year: 2008

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## **MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis**

Hwang, D ; Zhang, N ; Lee, H ; Yi, E ; Zhang, H ; Lee, I Y ; Hood, L ; Aebersold, R

**Abstract:** Summary: MS-BID (MS Biomarker Discovery Platform) is an integrative computational pipeline for biomarker discovery using LC-MS-based comparative proteomic analysis. This platform consists of several computational tools for: (i) detecting peptides in the collected patterns; (ii) matching detected peptides across a number of LC-MS datasets and (iii) selecting discriminatory peptides between classes of samples. Availability: MS-BID source codes, binaries and documentations are freely available under LGPL from <http://tools.proteomecenter.org/msBID.php>. Contact: [dhhwang@postech.ac.kr](mailto:dhhwang@postech.ac.kr)

DOI: <https://doi.org/10.1093/bioinformatics/btn491>

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ZORA URL: <https://doi.org/10.5167/uzh-155613>

Journal Article

Published Version

Originally published at:

Hwang, D; Zhang, N; Lee, H; Yi, E; Zhang, H; Lee, I Y; Hood, L; Aebersold, R (2008). MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis. *Bioinformatics*, 24(22):2641-2642.

DOI: <https://doi.org/10.1093/bioinformatics/btn491>

## MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis

Daehee Hwang<sup>1,2,\*†</sup>, Ning Zhang<sup>1,†</sup>, Hookeun Lee<sup>1,3</sup>, Eugene Yi<sup>1</sup>, Hui Zhang<sup>1</sup>, Inyoul Y. Lee<sup>1</sup>, Leroy Hood<sup>1</sup> and Ruedi Aebersold<sup>1,4,5</sup>

<sup>1</sup>Institute for Systems Biology, Seattle, WA 98103, USA, <sup>2</sup>I-BIO Program and Department of Chemical Eng., Pohang 790-784, <sup>3</sup>LCDI, Gachon University of Medicine and Science, Incheon, Republic of Korea, <sup>4</sup>Institute for Molecular Systems Biology, ETH, CH-8093 Zürich and <sup>5</sup>Faculty of natural science, University of Zürich, Zürich, Switzerland

Received on May 25, 2008; revised on September 2, 2008; accepted on September 12, 2008

Advance Access publication September 19, 2008

Associate Editor: John Quackenbush

### ABSTRACT

**Summary:** MS-BID (MS Biomarker Discovery Platform) is an integrative computational pipeline for biomarker discovery using LC-MS-based comparative proteomic analysis. This platform consists of several computational tools for: (i) detecting peptides in the collected patterns; (ii) matching detected peptides across a number of LC-MS datasets and (iii) selecting discriminatory peptides between classes of samples.

**Availability:** MS-BID source codes, binaries and documentations are freely available under LGPL from <http://tools.proteomecenter.org/msBID.php>.

**Contact:** dhhwang@postech.ac.kr

### 1 INTRODUCTION

Advances in quantitative proteomic analysis have offered new opportunities for identifying biomarker proteins in tissue and body fluid samples (Aebersold and Mann, 2003). However, proteomic analysis of such samples is still challenging due to both high sample complexity and the large dynamic range of protein concentrations (Anderson *et al.*, 2004). Therefore, no common proteomics technology has the capacity to completely analyze the entire complex proteome in biological samples. To increase the size of proteome detected from such samples, several sensitive, highly reproducible LC-MS approaches have been introduced (Mueller *et al.*, 2007). Despite highly reproducible LC-MS patterns from recent LC-MS technologies, the differences in LC-MS patterns that can arise from imperfect chromatography, contaminants, and ion suppression effects can still complicate the detection and matching of signals in and between samples. Therefore, there has been a need for a computational framework that can reliably: (i) detect peptides, (ii) match the corresponding peptides across multiple LC-MS data and (iii) select discriminatory peptides. Here, we present MS-BID, a Java package including a set of computational tools, which effectively achieves the above three tasks.

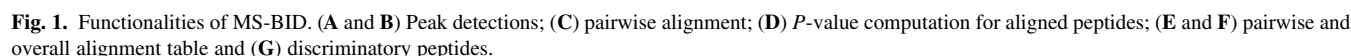
### 2 METHODS AND FEATURES

The features included in MS-BID are summarized in the following paragraphs. The MS-BID features were demonstrated using the datasets generated by QStar for three classes of mixtures consisting of nine proteins at known different molar ratios. The results (Fig. 1) show that MS-BID correctly selected the proteins whose abundances were varied across samples and accurately captured their relative ratios under the three conditions.

- Detection of peptide features: the data ( $m/z$  and intensity) for each scan (retention time) is extracted after converting LC-MS data to the mzXML format (Pedrioli *et al.*, 2004). In the entire dataset, a peptide with the largest intensity is first identified (the circled peptide in Fig. 1A). If the maximum intensity (the second isotopic peak in Fig. 1B) is larger than a cutoff value (by default, 25) and the charge state is between two and five, we statistically determine both ranges of  $m/z$  and retention time for the corresponding peptide feature using cumulative sum-based tests (Hamilton, 1994). The cutoff value can be adjusted considering the noise level in the data. We recommend setting the value as the highest noise level in the data.
- Determination of charge states: all isotopic peaks (local maxima numbered in Fig. 1B) for each detected peptide are first found using local maxima detection algorithm after smoothing the intensities five times using a convolution filter [1/3 1/3 1/3], and adjusting the  $m/z$  shifts coming from smoothing. A charge state is then assigned to each  $m/z$  distance between two consecutive isotopic peaks (the table in Fig. 1B), and a non-parametric voting scheme was used to determine the peptide charge state as the most frequently occurring one.
- Alignment of peptide features from multiple LC-MS experiments:
  1. *Pairwise alignments:* the following iterative pairwise alignment is done for each of all possible pairs of LC-MS experiments. For a particular pair of experiments ( $i$  and  $j$ ), each peptide detected in experiment  $i$  is initially matched with one of peptides with the same charge states in experiment  $j$ , such that this peptide pair has the shortest weighted Euclidean distance in  $m/z$  and retention time space (see two circled peptides linked by the dashed line in Fig. 1C). The weights are iteratively determined by minimizing the sum of weighted distances for the matched peptides. When MS/MS analysis is done for peptide sequencing, MS-BID also provides an optional procedure with which the identified peptides from MS2 can be matched if they are within the  $m/z$  range of 0.01 Da of the extracted features and reside in the elution profile of extracted features. Finally, the probability that each pair of matched peptides is matched by chance is computed using an empirical probability density function (PDF) of the weighted distance for random pairs

\*To whom correspondence should be addressed.

†The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.



2. *Overall alignment*: the overall alignment table is generated (Fig. 1F) by combining all sets of pairwise aligned peptides. Due to various reasons such as co-eluting peptides, some peptide features can fail to be detected. MS-BID provides an optional procedure that can estimate the intensities of the missing peptides. For a set of aligned peptides with a missing peptide (i.e. a row of alignment table in Fig. 1F with a missing value), MB-BID extracts the intensities within the range of  $m/z$  and retention time defined by the other aligned peptides from the mzXML file of the sample including the missing value and then fills in the intensity of the missing peptide using the highest intensity in the range. We made this procedure optional because it takes a long time when there are many missing peptides. Also, to reduce the computation time, MS-BID only searches for the peptides whose maximum intensities are larger than a cutoff (by default, 25). A few of hundreds of missing peptides were identified by this procedure from several datasets recently tested. The overall  $P$ -value for each set of matched peptides in the overall alignment table is computed using Fisher's method (Hwang *et al.*, 2005). To alleviate the variations from sample preparation, the intensities of each aligned feature are normalized such that the sums of the intensities of the top 10 peptides are to be the same in all the samples.

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